```
SEQUENCE FROM N.A.
STRAIN-WISTAR; TISSUE-BRAIN;
Russell F.D., Koishi K., Jiang Y., McLennan I.S.;
Russell F.D., Koishi K., Jiang Y., McLennan I.S.;
Anterograde axonal transport of glial cell line-derived neurotrophic factor and its receptors in rat hypoglossal nerve.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF205715; AAF23769.1;
NON_TER 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAINWISTAR; TISSUE-BRAIN;
STRAINWISTAR; TISSUE-BRAIN;
STRAINWISTAR; TISSUE-BRAIN;
STRAINWISTAR; TISSUE-BRAIN;
"Anterograde axonal transport of glial cell line-derived neurotrophic factor and its receptors in rat hypoglossal nerve.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF205714; ARF23768.1; -.
NON_TER 99 99
SEQUENCE 99 AA; 11025 MW; C60C998CD9C58723 CRC64;
                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GDNF splice variant 3 (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ENT splice variant 1 (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 99; DB 11; Length 99;
Pred. No. 6.5e-08;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 AA; 8262 MW; D6394FE64FFC67AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               090xJ8 PRELIMINARY; PRT; 99 AA. 090xJ8; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) GDNF splice variant 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 99; DB 11;
Pred. No. 4.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.2%; Sco. 94.7%; Pred. No. ...
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Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NPENSRGKGRRGQRGKNRG 19
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Matches 18; Conservative
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                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   090XJ9
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         ACCOCCOS REPRESENTATION OF THE PROPERTY OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Zhang B., Feng Z., Zhou Y., Peng X., Yuan J., Olang B.;
Submitted (ANG-2011) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AY052832; AALI1017.1;
InterPro; IPR001839; TGFb.
Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 AA; 20885 MW; 1988C50DA5EA1B10 CRC64;
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                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Glial cell-derived neurotrophic factor isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 104; DB 4;
100.0%; Pred. No. 2.2e-08;
tive 0; Mismatches 0;
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   185 AA.
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Cres 01-MAY-1999 (TrEMBLrel. 10, Las) 01-MAX-2002 (TrEMBLrel. 20, Las) Neurotrophic factor (Fragment).
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Matches 19; Conservative
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PRELIMINARY;
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Matches 18; Conserv
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SEQUENCE FROM N.A.
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ID 090xJ7
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Gaps

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Gaps

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 30, 2002, 15:40:57; Search time 29 Seconds

(without alignments)

134.996 Million cell updates/sec

Title:
Perfect score: 104
Sequence: 1 NPENSRGKGRRGORGKNRG 19
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Actal number of hits satisfying chosen parameters: 671580
```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:
SprREMBL_21:*
1: Sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_human:*
5: sp_human:*
6: sp_nammal:*
7: sp_mhc:*
8: sp_page:*
10: sp_phage:*
10: sp_phage:*
11: sp_rodent:*
12: sp_virus:*
13: sp_virus:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rvirus:* sp_bacteriap:*

sp_archeap:*

SUMMARIES

Description	09ud32 homo sapien	096144 homo sapien		Q9qxj7 rattus norv	O9dx18 rattus norv	09dx19 rattus norv	O8r485 rattus norv	Ogiam2 gallus gall	Q91am3 qallus qall	Q8qqe9 nipponia ni	091vpl arabidopsis	Q9aty5 arabidopsis			O8s6k4 oryza sativ	
ID	Q9UD32	Q96L44	097685	75XQ6Q	9CX060	65X060 .	Q8R485	091AM2	09IAM3	1 Q8QGE9	09LVP1	O9ATY5	O9LRT2	0 Q8RZE5	OBS6K4	089163
th DB	3 4	5 4	9 09	3 11	11 60	55 11	11 60	12 13	5 13	13 13	36 10	79 10	22 10	3 10	15 10	12
å Duery Match Length DB	13	37	160	-		H	ä	ä	2	14	6	147	152	5	Š	292
Ouery Match	100.0	100.0	97.1	95.2	95.2	95.2	95.2	69.2	69.2	68.3	57.7	55.8	55.8	54.8	53.4	53.4
Score	104	104	101	66	66	66	66	72	72	71	9	58	28	57	55.5	55.5
Result No.	-	7	e	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16

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21 NPENSRGKGRRGQRGKNRG 39

q

RESULT 2 Q96L44

Q9jgn8 rice grassy 09a749 caulobacter		Q94Iw2 oryza sativ	Q9vwf2 drosoph1la	Q91pq8 cynomolgus	Q9nka5 drosophila	Q9c2k5 neurospora	Q8uq82 agrobacteri		Q9c7yl arabidopsis			Q99da5 human 1mmun	human	human	O91140 human 1mmun		human		091170 human immun		Q9ync6 human immun	human		Q99z38 streptococc		Q9sfy4 arabidopsis	
09JGNB 09A749	094605	094 IW2	Q9VWF2	Q9 I PQ8	O9NKA5	Q9C2K5	Q80G82	Q9LPK1	09C7Y1	Q9FH39	099DC5	099DA5	Q99DA0	091136	091140	091144	091152	O9YNC9	091170	Q9YNC7	09YNC6	091180	0900Y9	099238	951287	09SFY4	Q9MAU9
12	10	10	'n	12	Ŋ	m	16	10	10	10	15	15	15	15	15	15	15	15	15	15	15	15	15	16	7	10	10
2925 898	161	350	2006	588	449	516	750	1207	1334	1334	100	100	100	100	100	100	100	100	100	100	100	100	100	539	669	1840	361
53.4	51.4	51.0	51.0	50.0	49.0	49.0	49.0	49.0	49.0	49.0	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	47.6
55.5	53.5	53	53	52	51	51	51	51	51	51	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	49.5
17	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43,	4	45

ALIGNMENTS

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Gaps
                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-95172201; Pubmed-7867768;
Schaar D.G., Steber B.A., Sherwood A.C., Dean D., Mendoza G.,
Ramakrishnan L., Dreyfus C.F., Black I.B.;
"Multiple astrocyte transcripts encode nigral trophic factors in rat
and human.";
                                                                                              Homo sapiens (Human).
Sukaryota i Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                              Length 133;
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                    133 AA; 14736 MW; B46B96DD5F679769 CRC64;
                                             Score 104; DB 4;
Pred. No. 1.5e-08;
); Mismatches 0;
                                                                                                                                                                                                                             EXP. Neurol. 130:387-393(1994).
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
HSSP; Q07731; 1AGQ.
Interpro; PF001839; TGFb.
Pfam; PF00019; TGF-beta; 1.
                         133 AA
                        PRT;
                                                                                                                                                                                                                                                                                                                                           100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                           1 NPENSRGKGRRGQRGKNRG 19
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 19; Conservative
                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                         Glycoprotein.
SEQUENCE 13
                      090D32
090D32;
RESULT 1
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Euteleostomi;

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Fukuda T., Sumiyoshi T., Takahashi M., Kataoka T., Asahara T., Inui H., Watatani M., Yasutomi M., Kamada N., Miyagawa K.; Inui H., Watatani M., Yasutomi M., Kamada N., Miyagawa K.; "Alterations of the double-strand break repair gene MREII in cancer."; Cancer Res. 61.23-26(2001).

-I- FUNCTION: Involved in DNA double-strand break repair (DSBR).

Possesses single-strand endonuclease activity and double-strand-specific 3'-5' exonuclease activity. Also involved in meiotic DSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paull T.T., Gellert M.; "The 3' to 5' exonuclease activity of Mre 11 facilitates repair of DNA double-strand breaks.";
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-1- SUBUNIT: FORMS A COMPLEX WITH RAD50 (By similarity).
-1- SUBCELLULAR LOCATION: Nuclear.
-1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-1- DISEASE: DEFECTS IN MRELIA ARE A CAUSE OF ATAXIA-TELANGIECTASIA-LIKE DISORDER (ATLD). IT IS A DISEASE WITH THE SAME CLINICAL FEATURE THAN ATAXIA-TELANGIECTASIA BUT WITH A SOMEWHAT MILDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20077641; PubMed-10612394; Stewart G.S., Maser R.S., Stankovic T., Bressan D.A., Kaplan M.I., Jaspers N.G.J., Raams A., Byrd P.J., Petrini J.H.J., Taylor A.M.R.; "The DNA double-strand break repair gene hMRE11 is mutated in individuals with an ataxia-telangiectasia-like disorder."; Cell 99:577-587(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petrini J.H.J., Walsh M.E., Dimare C., Chen X.-N., Korenberg J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pitts S.A., Kullar H.S., Stankovic T., Stewart G.S., Last J.I.K., Bedenham T., Armstrong S.J., Plane M., Chessa L., Taylor A.M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO C-TERMINUS.
Petrini J.H.J., Walsh M.E., Dimare C., Chen X.-N., Korenberg J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and characterization of the human MRE11 homologue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'MRE11: genomic structure and a null mutation identified in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1). Chamankhah M., Wei Y., Xiao W.;
"Molecular cloning and functional characterization of hNGS1,
                             01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Double-strand break repair protein MREIIA (MREII homolog 1).
MREIIA OR MREII OR HNGSI.
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcript protected from nonsense-mediated mRNA decay."; Hum. Mol. Genet. 10:1155-1162(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and human MRE11 homolog.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
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MEDLINE-21264328; Pubmed-11371508;
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE-96079094; PubMed-8530104;
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MEDLINE-98315380; PubMed-9651580;
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                                                                                                                                                                                                                Homo sapiens (Human)
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                                   between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB 1; Length 708; Pred. No. 1.8;
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R -> H (IN CANCER).
/FTId=var_011627.
R -> Q (IN CANCER).
/FTId=var_011628.
V -> A (IN REF. 1).
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N -> S (IN ATLD).
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M -> V.
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InterPro; IPR004843; M_ppestrase.
InterPro; IPR004844; S/T_phosphtse.
Pfam; PF00149; Metallophos; I.
TIGRRAMS; TIGR00583; mrell; I.
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VARSPLIC 595 622 MI
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80593 MW;
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AF073362; AAC36249
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nes 10; Conserv
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AF303388;
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ILF3_HUMAN
                                                                                                                                                                                                                                                                                                                   EMBL;
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EMBL;
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3D-structure.
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MR11_HUMAN
ID MR11_HUMAN
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CONFLICT
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CARBOHYD
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-50 FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN-WAStar; TISSUE-Kidney;
STRAIN-WASTACO, Pubmed-7696586;
Suter-Crazzolara C., Unsicker K.;
"GDNF is expressed in two forms in many tissues outside the CNS.";
NeuroReport 5:2486-2488(1994).
                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
GRRILEAPAEDHSLGHRRVPFALITSDS -> A (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93262463; PubMed-8493557;
Lin L.-F.H., Doherty D.H., Lile J.D., Bektesh S., Collins F.;
"GDNF: a glial cell line-derived neurotrophic factor for midbrain
                                                                                                                                                                                                                                                             BY SIMILARITY.
GLIAL CELL LINE-DERIVED NEUROTROPHIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Springer J.E., Seeburger J.L., He J., Gabrea A., Blankenhorn E.P. Bergman L.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 211;
                                                                                                                                                                                                           FALSE_NEG.
Signal; Alternative splicing.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 78-102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   B6731C767A3A95B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDNF_RAT STANDARD; PRT; 211 AA. 007731; 064062; 064063; 063214; 01-FEB-1995 (Ral. 31, Created) 01-FEB-1995 (Ral. 31, Last sequence update) 16-OCT-2001 (Ral. 40, Last annotation update) Glial cell line-derived neurotrophic factor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.2%; Score 99; DB 1; I 94.7%; Pred. No. 2.1e-07; Live 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
MEDLINE-95203379; PubMed-7895811;
                                                                                                                                                     InterPro; IPR001839; TGFb.
Pfam; PF00019; TGF-beta; 1.
SMART; SM00204; TGFB: 1.
PROSITE; PS00250; TGF_BETA_1;
Growth factor; Glycoprotein; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                   23662 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exp. Neurol. 131:47-52(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 260:1130-1132(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPENSRGKGRRGQRGKNRG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                               211
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Best Local Similarity (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 AA;
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                                                                                                                                           MGD; MGI:107430;
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                                                                                     D88352; 1
D88351; 1
Q07731;
                                                     U36449;
D88264;
                                     D49921;
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EMBL;
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HSSP;
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                                         EMBL;
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   REAR REPAREMENT OF THE PROPERTY OF THE PROPERT
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                                                                     "Multiple astrocyte transcripts encode nigral trophic factors in rat and human.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
GKRLLEAPAEDHSLGHRRVPFALTSDS -> A (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR.
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                                     Schaar D.G., Steber B.A., Sherwood A.C., Dean D., Mendoza G.
Ramakrishnan L., Dreyfus C.F., Black I.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --> S (IN REF. 2).
-> K (IN REF. 2).
-> D (IN REF. 1; AA SEQUENCE)
AE06C646682895AS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.2%; Score 99; DB 1; Length 211; 94.7%; Pred. No. 2.1e-07; 1ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00250; TGF_BETA_1; FALSE_NEG.
Growth factor; Glycoprotein; Signal; Alternative splicing;
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ALTERNATIVE SPLICING.
MEDLINE-95172201; PubMed-7867768;
                                                                                                  Exp. Neurol. 130:387-393(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L15305; AAA67909.1; --
EMBL; S75583; AAB33891.1; --
EMBL; S75583; AAB33892.1; --
EMBL; X92495; CAA63237.1; --
PIR; A37499; A37499.
PDB; 1AGO; O5-UN-97.
Interpro; IPRO01839; TGFb.
Pfam; PF00019; TGF-beta; 1.
SMART; SM00204; TGF-b
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Best Local Similarity 94.73
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                          Lyonnet S.; ^{\circ} Germline mutations of the RET ligand GDNF are not sufficient to cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTESTINAL OBSTRUCTION.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY, GDNF SUBFAMILY.
DATABASE: NAME-RED Systems, cytokine mini-reviews: GDNF;
WWW-"http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId-201".
                                                                                                                                                                                                                                                                                                                                                           ORDERIOR NUCLEOR AND MORPHOLOGICAL DIFFERENTIATION OF DOPAMINERGIC NEURONS AND MORPHOLOGICAL DIFFERENTIATION OF DOPAMINE UPTAKE.

1 CNERAGES THEIR HIGH-AFFINITY DOPAMINE UPTAKE.

1 SUBGUIT: HOMODIMER: DISULFIDE-LINKED.

1 SUBCELLULAR LOCATION: Secreted.

1 ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.

1 DISEASE: IN ASSOCIATION WITH MUTATIONS OF RET GENE, MAY BE INVOLVED IN HIRSCHSPRUNG'S DISEASE (HSCR). THIS GENETIC DISORDER OF NEURAL CREST DEVELOPMENT IS CHARACTERIZED BY THE ABSENCE OF INTRAMURAL GANGLION CELLS IN THE HINDGUT; OFTEN RESULTING IN INTESTINAL OBSTRUCTION.
                                                                                                       MEDLINE-97051933; PubMed-8896568; Angrist M., Bolk S., Halushka M., Lapchak P.A., Chakravarti A.; Angrist M., Bolk S., Halushka M., Lapchak P.A., Chakravarti A.; Germilne mutations in glial cell line-derived neurotrophic factor (GDNF) and RET in a Hirschsprung disease patient."; Nat. Genet. 14:341-344(1996).
Ivanchuk S.M., Myers S.M., Eng C., Mulligan L.M.;
De novo mutation of GDNF, ligand for the RET/GDNFR-alpha receptor complex, in Hirschsprung disease.";
Hum. Mol. Genet. 5:2023-2026(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
GKRPPEAPAEDRSLGRRRAPFALSSDS -> A (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
GLIAL CELL LINE-DERIVED NEUROTROPHIC
FACTOR.
                                                                                                                                                                                                                   VARIANTS HSCR SER-21 AND ASN-150.
MEDLINE-97051934; PubMed-8895569;
Salomon R., Attie T., Pelet A., Bidaud C., Eng C., Amiel J.,
Sarnacki S., Goulet O., Ricour C., Nihoul-Fekete C., Munnich A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth factor; Glycoprotein; Signal; Alternative splicing; Polymorphism; Disease mutation; Hirschsprung disease. SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR01839; TGFD.
Pfam; PF00019; TGF- beta; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; FALSE_NEG.
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EMBL; L19062; AAA67910.1; JOINED.
EMBL, AF053748; AAD43139.1; -.
PIR; B37499; B37499.
HSSP; Q07731; 1AGQ.
Genew; HGNC:4232; GDNF.
                                                                                                                                                                                                                                                                                                                            Hirschsprung disease.";
Nat. Genet. 14:345-347(1996).
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                                                                                            VARIANT HSCR TRP-93.
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                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
R -> W (IN HSCR; ASSOCIATED TO A RET
MUTATION; COULD BE AN EXTREMELY RARE
POLYMORPHISM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sakai O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: Secreted.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. GDNF SUBFAMILY.
                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsushita N., Fujita Y., Nagatsu T., Kluchi K.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NEUROPROPHIC FORTOR THAT ENHANCES SURVIVAL AND
MORPHOLOGICAL DIFFERENTIATION OF DOPAMINERGIC NEURONS AND
INCREASES THEIR HIGH-AFFINITY DOPAMINE UPTAKE.
-!- SUBUNIT: HOMODIMER; DISULFIDE_LINKED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ICR; TISSUE-Dorsal root ganglion;
MEDILINE-9379105; PubMed-7650763;
Watabe K., Fukuda T., Tanaka J., Honda H., Toyohara K., Sakal
"Spontaneously immortalized adult mouse Schwann cells secrete
autocrine and paractine growth-promoting activities.";
J. Neurosci. Res. 41:279-290(1995).
                                           /FTId=VAR_009495.
D -> N (IN HSCR; COULD BE A POLKWORPHISM).
/FTId=VAR_009496.
T -> S (IN HSCR; SPORADIC FORM).
/FTId=VAR_009497.
                                                                                                                                                                                        100.0%; Score 104; DB 1; Length 211; 100.0%; Pred. No. 4e-08;
                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
STRALM-CS/BL/10J; TISSUE-Brain;
WANG F., Too H.P.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                 948540; P97919; 009058; P97920; P70446; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Glial cell line-derived neurotrophic factor precursor.
                                                                                                                                                     A0D1EBF77FC82691 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        211 AA.
                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                     211 AA; 23720 MW;
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                                                                                                                                                                                                          Best Local Similarity 100.
Matches 19; Conservative
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93
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93
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                                                                                                                                                       SEQUENCE
                                                                                                                                                                                          Query Match
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GDNF_MOUSE
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EMBL; U37459; AAB18672.1; ALT_INIT.

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

December 30, 2002, 15:38:52; Search time 11 Seconds (without alignments) 71.641 Million cell updates/sec Run on:

US-09-687-993-18 104 1 NPENSRGKGRRGQRGKNRG 19

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 otal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	. B	mus m	Q07731 rattus norv	P49959 homo sapien	Q12906 h interleuk	Q9jil3 rattus norv	Q9z1x4 mus musculu	P32505 saccharomyc	043992 leishmania		P44586 haemophilus				Q10013 caenorhabdi	Q59749 rhizobium m		Q61216 mus musculu	O83244 treponema p	homo sapie	Q00684 saccharomyc	Q06787 homo sapien			P31612 wound tumor		P52157 streptomyce	Q9z321 mus musculu	P38912 saccharomyc			m	Q9xgm2 arabidopsis
SUMMARIES	ID	DNF	GDNF_MOUSE	GDNF_RAT	MR11_HUMAN	ILF3_HUMAN	ILF3_RAT	ILF3_MOUSE	NAB2_YEAST	RS2_LEIAM	LRP1_HSV1F	DEAD_HAEIN	VE2_HPV12	ROR_HUMAN	YK09_CAEEL	SMD1_CAEEL	PARC_RHIME	SMD1_SCHPO	MR11_MOUSE	Y214_TREPA	FBRL_HUMAN	CC14_YEAST	FMR1_HUMAN	MR11_RAT	LSM4_CAEEL	VP12_WTVNJ	RS2_SCHPO	RHO_STRLI	TP3B_MOUSE	IFIA_YEAST	NSR1_YEAST	MR11_CHICK	×	MR11_ARATH
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	Length		211	21	70	8	91	91	52	26	34	61	49	633	64	.12	758	1	70	9	32	55	63	70	12	17	25	70	96	15	41	700	48	72
ď	Ouery Match	0	95.2	'n	Н.	a,	σ	49.5	49.0	48.1	œ	48.1	47.1	46,6	9	46.2	9	45.7	45.2			44.2										3		
	Score	10	66	66	in		51.5		51	20	20	20	49	٠	48.5	48	4	47.5	47	46	46	46	46	₹.	45.5	45	4.5	4.5	45	4.	4	44.5	44	44
	Result No.		C4	m	4	'n	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	58	30	31	32	33

homo saplen saccharomyc xenopus lae rattus norv mus musculu caenorhabdi drosophila neisseria m neisseria m epstein-bar human papil
015027 P20082 009003 P13941 P34486 021724 091729 P12978 P26545
CEB1_HUMAN SNF2_YEAST SPH1_XENLA CA13_RAT CA13_MOUSE YMJA_CAEEL CA2_DROME PURA_NEIMA PURA_NEIMB EBN2_EBV VE2_HPV5B
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740 1703 536 636 1464 404 432 432 432 432 632 514
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ALIGNMENTS

GDNF_HUMAN P39905; Q9UP9	STANDARD; 7; Q9UD33;	PRT;	211 AA.		
01-FEB-1995 (Rel. 01-FEB-1995 (Rel. 16-OCT-2001 (Rel.	(Rel. 31, Created) (Rel. 31, Last sequence update) (Rel. 40, Last annotation undat	ed) sequence	update)	-	
Glial cell line-derived derived trophic factor	Glial cell line-derived neurotrophic derived trophic factor 1) (ATF-1).	neurotrophic 1) (ATF-1).	factor	precursor	factor precursor (Astrocyte-
GDNF.					
Homo sapiens (Human) Fukarvota: Metazoa:	(Human). Tazoa: Chordatz	r. Cranta	.a. Vert	Phrata: E	Cranjata: Vertebrata: Euteleostomi:
Mammalia, Eut	Eutherla; Primates;	3; Catarr	lait; Ho	Catarrhini, Hominidae,	Homo.
NCBI_TaxID=9606;	06;				
SEQUENCE FROM	N.A. (ISOFORM	1).			
MEDLINE-93262	463; PubMed-849	13557;			
Lin LF.H.,	Lin LF.H., Doherty D.H., Lile J.D., Bektesh	ille J.D.	Bektes	S., Col	lins F.;
GDNF: a glia	i cell line-der pourong ".	ived neu	rotropu	ractor	ror midbrain
Science 260:1	Science 260:1130-1132(1993).				
[2]	•				
SEQUENCE FROM	SEQUENCE FROM N.A. (ISOFORM 2).	2).			
MEDLINE-95172	201; PubMed-786	57768;			:
Schaar D.G.,	Sleber B.A., Sherwood A.C.,	erwood A		ın D., Mendoza	doza G.,
Ramakrishnan "Multiple aet	Ramakrishnan L., Dreytus C.F., Black I.B.; "Multiple setrocute transcripts encode ploral	F., Black	I.B.;		
and human.";	rocyte transcr	oons end	orfirm ar		ractors in rac
Exp. Neurol.	Exp. Neurol. 130:387-393(1994)	34).			
[3]					-
SEQUENCE OF 1	SEQUENCE OF 1-187 FROM N.A. (ISOFORM	(ISOFORM	1).		
TISSUE-Kidney;	TISSUE=Kidney; MFD::INF=00206655: DubMed=10366742;	. 64243.			
Baecker P.A., Lee	Lee W.H. Verity A.N.	_	Ealen	M. John	
"Characteriza	"Characterization of a promoter for		the hums	the human glial cell	cll line-derived
neurotrophic factor	factor gene.";			,	
Brain Res. Mo	Brain Res. Mol. Brain Res. 69:209-222(1999)	59:209-22	2(1999)		
[4]					
PARTIAL SEQUENCE,		TIDE BOND			
MEDLINE-97141760;		38018;			
Haniu M., Hui J.,	J., Young Y., Le J., Katta V.,	Le J., K	atta V.,	Lee R.,	Shimamoto G.,
Konde M.F.				•	
"Glial cell I	line-derived ned	neurotrophic factor:	tacto	: selecti	7 h
diamifide atr	the intermolectiar disullide linkage disulfide structure ":	s tinkage	and cna	and characterization of	tion of its
Blochemistry	35:16799-16805	.19861			
[5]		. ()			
REVIEW ON VARIANTS.	IANTS.				
MEDLINE-98023		59036;			
Hofstra R.M.W	Hofstra R.M.W., Osinga J., I		Σ.		
"Mutations in		disease:	when does	43	mutation contribute
phenotype					
. J. Hum.	Genet. 5:180-185(1997)	35(1997).			
[6]					
VARIANI ROCK SEK-104	SEK-ID4.				

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Gaps

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Tibonuclease, Rne/Rng family protein [imported] - Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Date: 20-Apr-2001
#sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C; Accession: H87481
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B; Laub, W.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                       C;Species: rice grassy stunt virus
C;Species: rice grassy stunt virus
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C;Accession: T00133
N;Toriyama, S; Kimishima, T; Takahashi, M.; Shimizu, T.; Minaka, N.; Akutsu, K.
J. Gen. Virol. 79, 2051-2058, 1998
A;Title: The complete nucleotide sequence of the rice grassy stunt virus genome and gA;Title: The complete nucleotide sequence of the rice grassy stunt virus genome and gA;Teference number: 214118; MUID:98378059; PMID:9714257
A;Accession: T00133
A;Status: translated from GB/EMBL/DDBJ
A;Accession: T00133
A;Status: 1.2925 crops
A;Residues: 1.2925 crops
A;Residues: 1.2925 crops
A;Cross-references: EMBL:AB009656; NID:g3410897; PIDN:BAA32246.1; PID:g3410899
A;Experimental source: isolate IRRI
C;Keywords: nucleotidyltransferase
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FNA-binding protein NAB2 - yeast (Saccharomyces cerevisiae)

FNA-binding protein NAB2 - yeast (Saccharomyces cerevisiae)

FNA-binding protein G3910; protein G312c

C; Species: Saccharomyces cerevisiae

C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000

C; Accession: B48058; A48058; S64132

FR: Anderson, J.T.; Wilson, S.M.; Datar, K.V.; Swanson, M.S.

Mol. Cell. Biol. 13, 2730-2741, 1993

A; Title: NAB2: a yeast nuclear polyadenylated RNA-binding protein essential for cell

A; Recession: B48058

A; Molecule type: DNA

A; Residues: 1-525 < AND>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:L10288; NID:9295628; PIDN:AAA34819.1; PID:9295629
                                                                                                                                                               (EC 2.7.7.48) - rice grassy stunt virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2925;
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5.5;
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2907 NPPSSRGRGRRG-RGRS 2922
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                   RNA-directed RNA
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F;1-211/Product: glial cell line-derived neurotrophic factor splice form GDNF633 #status
F;1-24/**, 52-211/Product: glial cell line-derived neurotrophic factor splice form GDNFF
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-7/Domain: propeptide #status predicted <PRO>
F;20-7/Domain: propeptide #status predicted <PRO>
F;78-211/Product: glial cell line-derived neurotrophic factor #status experimental <MAT>
F;126,162/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glial cell line-derived neuotrophic factor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
C;Accession: 149686; JC6518
R;Watabe, K.; Fukuda, T.; Tanaka, J.; Honda, H.; Toyohara, K.; Sakal, O.
Neuroscl. Res. 41, 279-290, 1995
Title: Spontaneously immortalized adult mouse Schwann cells secrete autocrine and para
K;Reference number: 149686; MUID:95379105; PMID:7650763
A;Accession: 149686
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A.Molecule type: mRNA
A.Residues: 1-211 <RESS
A.Residues: 1-211 (RESS
A.Residues: 1-211 (RESS
B.Matsushita, N.; Fujita, Y.; Tanaka, M.; Nogatsu, T.; Kluchi, K.
Gene 203, 149-157, 1997
A.Title: Cloning and structural organization of the gene encoding the mouse glial cell
A.Reference number: JC6518; MUID:98086214; PMID:9426245
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                                                                                                   A Molecule type: mRNA

A Residues: 1-24 'A', 52-76 'S', 78-89, 'K', 91-211 <SPR1>
A Cross-references: GB:S75585; NID:9912790; PIDN:AB33892.1; PID:9912791
A Crossion: 153427
A Accession: 153427
A Accession: 153427
A Accession: 153427
A Residues: 1-76 'S', 78-89, 'K', 91-211 <SPR2>
A References: GB:S7583; NID:9912789; PIDN:AAB33891.1; PID:9912789
A Reference of the type: SPR2 'STR2 '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holecule type: mRNA
Regidues: 1-24,74,75-76 SSUT>
Regidues: T-24,74,75-76 SSUT>
Roros references: EMBL.X92495; NID:g1045219; PIDN:CAA63237.1; PID:g1045220
Experimental source: strain wistar; kidney
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Pred. No. 8.7e-07;
1; Mismatches 0; Indels
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A; Reference number: 153427; MUID:95203379; PMID:7895811
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Pred, No. 8.7e-07;
                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 94.7
Matches 18; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
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Gaps

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

December 30, 2002, 16:12:27; Search time 15 Seconds (without alignments) 121.770 Million cell updates/sec Run on:

104 1 NPENSRGKGRRGQRGKNRG 19 US-09-687-993-18 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

283224 tal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	qlial cell line-de		ze11	RNA-directed RNA p	ribonuclease, Rne/	RNA-binding protei	topoisomerase 1v c	topoisomerase IV s	probable copia-typ	latency-related pr	probable ATP-depen	hypothetical prote			E2 protein - human	70.5K hpothetical	heterogeneous nucl	hypothetical prote	small nuclear ribo	unknown protein, 4	dsRNA-binding prot	hypothetical prote		hypothetical prote	probable transcrip	hypothetical prote			9
SUMMARIES	ΩI	B37499	A37499	149686	T00133	H87481	B48058	A97501	AE2719	E86451	WMBEL1	F64056	T01458	АН1867	T39586 .	S36541	G88533	T02673	T16952	T38440	E96576	151652	T47841	JC7700	T49225	T42606	D96831	A96592	T05039	151653
	88	N	•	•	•	7	•	۲۹ -	C1	N	н _	7						7												
	Query Match Length DB	211	211	211	2925	868	525	750	750	1334	340	613	296	893	166	494	627	633	126	117	523	695	1339	269	300	536	959	848	1171	800
9 2	Ouery	100.0	95.2	95.2	53.4	51.9		49.0	49.0	49.0	48.1	٠	47.6	47.6	47.1	47.1	46.6	46.6		45.7	45.7	45.7	•		45.2	45.2	45.2	45.2	45.2	44.7
	Score	104	66	66	55.5	54	51	51	51		20	20	6	•	49	49	ω.	48.5	48	47.5	47.5		47.5	47	47	47	47	47	47	46.5
	Result No.	7	7	3	4	S	9	7	œ	6	10	1	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

	hypothetical prote		fibrillarin (valid	hypothetical prote	probable transcrip	oleosin-like prote	probable ATP-depen	probable ATP-depen	protein-tyrosine-p	fragile X mental r	hypothetical prote	probable qaq-pol p	T20H2,2 protein -	nonstructural prot	40s ribosomal prot
D86311	D71352	A96744	A38712	T31600	T12180	T08134	C90738	D85588	S56283	A40724	T16234	G86461	H86335	MNXR12	T41418
7	~	~	N	N	~	N	~	N	N	٦	N	~	~	-	7
1188	65	243	321	335	370	375	455	455	551	632	123	467	538	178	253
44.7	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	43.8	43.8	43.8	43.3	43.3
46.5	46	46	46	46	46	46	46	46	46	46	45.5	45.5	45.5	45	4
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 B31499
glial cell line-derived neurotrophic factor precursor · human
C.Species: Homo sapiens (man)
C;Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 26-Aug-1999
C; Accession: B37499
Rith, L.F.; Doherty, D.H.; Lile, J.D.; Bektesh, S.; Collins, F. Srience 260 1130-1132 1993
A;Title: GDNF: a qilal cell line-derived neurotrophic factor for midbrain donamineral
A; Reference number: A37499; MUID:93262463; PMID:8493557
A; Accession: B37499
A; Molecule type: DNA
A; Residues: 1-211 <lin></lin>
A; Cross-references: GB:L19063; GB:L15306; NID:g306761; PIDN:AAA67910.1; PID:g306763
A; Note: sequence extracted from NCBI backbone (NCBIP:132084)
C;Keywords: glycoprotein; homodimer
F;1-19/Domain: signal sequence #status predicted <sig></sig>
F;20-77/Domain: propeptide *status predicted <pro></pro>
F;78-211/Product: glial cell line-derived neurotrophic factor #status predicted <mat></mat>
F;126,162/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 104; DB 2; Length 211;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NPENSRGKGRRGQRGKNRG 19
======================================
Db 99 NPENSRGKGRRGQRGKNRG 117

Milal cell line-derived neurotrophic factor precursor - rat
Nichternate names: GNNF
Nichternates agilal cell line-derived neurotrophic factor splice form GDNF555; glial cel
Nicontanis: glial cell line-derived neurotrophic factor splice form GDNF555; glial ce
C; Species: Ratus norvegicus (Norway rat)
C; Date: 16-Feb-1994 #sequence_revision 16-Feb-1994 #text_change 05-Nov-1999
C; Cacession: A37499; MUID:93262463; PMID:8493557
A; Reference number: A37499; MUID:93262463; PMID:8493557

A; Molecule type: mRNA; protein
A; Residues: 1-211 <LIN>
A; Residues: 1-211 <LIN>
A; Residues: 1-211 <LIN>
A; Cross-references: GB:LL5305; NID:g310123; PIDN:AAA67909.1; PID:g310124
A; Experimental source: g1ial cell line B49
A; Note: sequence extracted from NCB1 backbone (NCBIP:132083)
A; Note: sequence extracted from NCB1 backbone (NCBIP:132083)
B; Springer, J.E.; Seeburger, J.L.; He, J.; Gabrea, A.; Blankenhorn, E.P.; Bergman, L. Exp. Neurol. 131, 47-52, 1995
A; Title: cDNA sequence and differential mRNA regulation of two forms of glial cell li

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Gaps

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0; Indels

Mismatches

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1 NPENSRGKGRRGQRGKNRG 19
     19; Conservative
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                                                                                                                      RESULT 15
US-08-535-681-32
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       Matches
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Patent No. 6184200

GENERAL INFORMATION:
APPLICANT: Hu, Sylvia
TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS: AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 32;
                                                                                                                                                                                                                                                                                                                                              Length 31;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,681
                                                                                                                                                                                                                                                                                                                                              Score 104; DB 4;
Pred. No. 6.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 104; DB 4;
Pred. No. 6.4e-09;
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
APPLICATION NUMBER: US/08/535,681
FILIG DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CULTY, Daniel R.
REGISTRATION NUMBER: 3-727
REFERENCE/DOCKET NUMBER: A-357
TELECHHONE: 805-447-8102
TELEPHONE: 805-499-8011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: AMGEN INC.
STREET: 1840 DeHavilland Drive
STRIT: Thousand Oaks
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                            100.0%; Sur
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: CULTY, DADIEL R.
REGISTRATION NUMBER: 32.727
REFERENCE/DOCKET NUMBER: A-35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
TELEPHONE: 805-499-8011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                               1 NPENSRGKGRRGQRGKNRG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                 13 NPENSRGKGRRGQRGKNRG 31
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-535-681-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-535-681-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91320
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                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hu, Sylvia
TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic
TITLE OF INVENTION: Factor
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN IN:
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
ZIP: 91320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,681
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 104; 100.0%; Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                      Sequence 32, Application US/08535681
Patent No. 6184200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/ACENT INFORMATION:
NAME: CLETY, Daniel R.
REGISTRATION NUMBER: 32,727
REFERENCE/POCKET NUMBER: A-35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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14 NPENSRGKGRRGQRGKNRG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 805-447-81
TELEFAX: 805-499-8011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-681-32
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Matches 19; Conserv
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1 NPENSRGKGRRGQRGKNRG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 805-499-8011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                STATE: California
COUNTRY: United Si
ZIP: 91320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 19; Conserv
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                         JS-08-535-681-29
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Sequence 28, Application US/08535681

Patent No. 6184410N:
GENERAL INFORMATION:
APPLICANT: Hu, Sylvia
TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic TITLE OF INVENTION: Factor
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: AMGEN INC.
STREPT: 1840 DeHavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Industic Jans
STATE: California
COUNTRY: United States of America
ZIP: 91320
COUNTRY: United States of America
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,681
FILING DATE:
CLASSIFICATION: S30
ATTORNEY/AGENT INFORMATION:
NAME: CULTY, Daniel R.
REGISTRATION NUMBER: 32,727
REPERBNICE/DOCKET NUMBER: 32,727
RECENENCE/DOCKET NUMBER: A-357
TELEPHONE: 805-447-8102
TELEFRAX: 805-447-8101
                                                                                                                                                                                                                                              100.0%; Score 104; DB 4; 100.0%; Pred. No. 5.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 104; DB 4;
Pred. No. 5.8e-09;
; Mismatches 0;
                                                                                                                                                                                                                                                                                   Mismatches
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TELECOMMUNICATION INFORMATION: TELEPHONE: 805-447-8102
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100.0%;
                                                                            27:
                                                                                                                                                                                                                                                                                                                                         10 NPENSRGKGRRGORGKNRG 28
                                                                    INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                      1 NPENSRGKGRRGQRGKNRG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 NPENSRGKGRRGQRGKNRG 19
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                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Conservative
                                     TELEFAX: 805-499-8011
                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-681-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-08-535-681-28
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UGS-08-335-681-39

UGS-08-335-681-30

UGS-08-335-68
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                                                                                                                                                                                                                                                                                                                      Gaps
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TITLE OF INVENTION: Factor
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: 50
Sequence 25, Aboress: Aboress: Aboressed US/08585651
Sequence 25, Aboressed US/0858651
Sequence 25, Aboressed US/0
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Patent No. 6184200
GENERAL INFORMATION:
APPLICANT: Hu, Sylvia
TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                       DB 4; Length 25;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,681
                                                                                                                                                                                                                                   100.0%; Score 104; DB 4 100.0%; Pred. No. 5e-09;
                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: AMGEN INC.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: CURTY, Daniel R.
REGISTRATION NUMBER: 32,727
RELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
TELEFAX: 805-499-8011
                                                                                                                                                                                                                                                                                                              ;
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SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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                        STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: peptide
US-08-535-681-24
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CLASSIFICATION: 530
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amino acid
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Sequence 27, Application US/08535681
Fatent No. 6184200
GENERAL INFORMATION:
TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic
TITLE OF INVENTION: Factor
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: AMGEN INC.
STREET: 1840 Deflavilland Drive
CITY: Thousand Oaks
STREET: California
COUNTRY: United States of America
ZIP: 91320
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                                        COUNTRY: AMGEN INC.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,681
FILING DATE:
CLASSIFICATION: SON
ATORNEY/AGENT INFORMATION:
NAME: CLITY, Daniel R.
REGISTRATION: MUMBER: 32,727
REGISTRATION NUMBER: 32,727
REGISTRATION NUMBER: 32,727
REGISTRATION NUMBER: 32,727
REGISTRATION NUMBER: 32,727
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTHAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 104; DB 4;
ilarity 100.0%; Pred. No. 5.4e-09;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CUTTY, Daniel R
REGISTRATION NUMBER: 32,727
REFERENCE/DOCKET NUMBER: A-357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: 805-447-8102
TELEFAX: 805-499-8011
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
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MOLECULE TYPE: peptide
US-08-535-681-26
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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US-08-535-681-24

Sequence 24, Application US/08535681

APPLICANT: Hu, Sylvia

TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic

TITLE OF INVENTION: Factor

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

STREET: 1840 DeHavilland Drive

CITY: Thousand Oaks

STATE: Callfornia

COUNTRY: United States of America

ZIP: 91320
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                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,681
FILING DATE:
CLASSIFICATION: 530
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APPLICATION NUMBER: US/08/535,681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 104; DB 4; 100.0%; Pred. No. 4.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
      United States of America
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: CURTY, Daniel R.
REGISTRATION NUMBER: 32,727
REFRENCE/COCKET NUMBER: 4-35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Curry, Daniel R.
REGISTRATION NUMBER: 32,727
REFRENCE/DOCKET NUMBER: A-35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 24 amino acids
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Matches 19; Conservative
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-535-681-23
      COUNTRY:
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Sequence 23, Application US/08535681

Type 24, Application: Truncated Glial Cell Line-Derived Neurotrophic TITLE OF INVENTION: Pactor NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS: AMGEN INC.

STREET: 1840 DeHavilland Drive

CITY: Thousand Oaks

STATE: California
                                                                                                                                                                                                                     Sequence 22, Application US/08535681

Patent No. 6184200
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic TITLE OF INVENTION: Factor NUMBER OF SEQUENCES: 50
CORRESPONDENCE AMGEN INC.
STREET: 1840 Dehavilland Drive CITY: Thousand Oaks
STATE: California
CONTRY: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREW! APPLICATION DATA:
APPLICATION NUMBER: US/08/535,681
100.0%; Pred. No. 4.4e-09; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 104; DB 4; 100.0%; Pred. No. 4.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CULTY, DANIEL R.
REGISTRATION NUMBER: 32,727
REFERENCE/DOCKET NUMBER: A-357
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
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                                                                     NPENSRGKGRRGQRGKNRG 19
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LENGTH: 23 amino acids
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Best Local Similarity 100.
Matches 19; Conservative
Best Local Similarity 100.
Matches 19; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
S-08-535-681-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
TELEFAX: 8
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                                                                                                                                                                                  RESULT 5
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US-08-535-681-21
Sequence 21, Application US/08535681
Sequence 21, Application US/085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 104; DB 4;
Pred. No. 4.2e-09;
.. wismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSE: AMGEN INC.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
ZIP: 91320
                            US/08/535,681
                                                                                  CLASSIFICATION: 530.
ATTORNEY/AGENT INFORMATION:
NAME: CULTY, Daniel R.
REGISTRATION NUMBER: 32,727
REFERENCE/DOCKET NUMBER: A-3:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
TELEFAX: 805-499-8011
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CULTY, DATIEL R.
REGISTRATION NUMBER: 32,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 NPENSRGKGRRGQRGKNRG 19
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
FIGNORM: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
POPOLOGY: linear
MOLECULE TYPE: peptide
US-08-535-681-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
CURRENT APPLICATION DATA
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TELEX:
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                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 19; Conserv
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                                                                            Sequence 19, Application US/08535681
Patent No. 6184200
GENERAL INFORMATION:
TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic TITLE OF INVENTION: Factor NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: AMGEN INC.
STREET: 1840 DeHavilland Drive CITY: Thousand Oaks
STRATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/08535681
Patent No. 6184200
GENERAL INFORMATION:
APPLICANT: Hu, Sylvia
TITLE OF INVENTION: Factor
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: AMGEN INC.
STREET: 1840 DeHavilland Drive
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Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATERITI Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/535,681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 104; Best Local Similarity 100.0%; Pred. No. 46 Matches 19; Conservative 0; Mismatches
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United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: CURTY, DANIEL R.
REGISTRATION NUMBER: 32.727
REFERENCE/DOCKET NUMBER: A-35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
TELEPHONE: 805-499-8011
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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TOPOLOGY: linear
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CLASSIFICATION: 530
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US-08-535-681-20
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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched

Minimum DB seq Maximum DB seq

Database

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Sequence 18, Application US/08535681
Patent No. 6184200
GENERAL INFORMATION:
APPLICANT: Hu, Sylvia
TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophic
TITLE OF INVENTION: Factor
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
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STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
ZIP: 91320
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PC COMPUTER: OCCUPATER: PE PC POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RELING DATE: OCCUPATER: US/08/535,681
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100.0%; Pred. No. 3.9e-09;
11ve 0; Mismatches 0;
US-08-618-543-1

US-08-742-035-76

US-08-777-019-76

US-08-606-176A-1

US-08-777-143-76

US-08-777-143-76

US-08-453-176A-6

US-08-453-176A-6

US-08-451-374-6

US-08-935-681-2

US-08-931-858E-76

US-08-931-858E-76
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ATVORNEY/AGENT INFORMATION:
NAME: CULTY, Daniel R.
REGISTRATION NUMBER: 32,727
REFERENCE/DOCKEY NUMBER: A-357
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805-447-8102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 18:
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TYPE: amino acid
STRANDEDNESS: single
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; MOLECULE TYPE: peptide
US-08-535-681-18
     Query Match
Best Local Similarity
Matches 19; Conserv
  US-08-535-681-18
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/FB_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/FB_COMB.pep:*
                       5.1.3
Compugen Ltd.
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US-08-535-681-19
US-08-535-681-21
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US-08-535-681-23
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US-08-535-681-25
US-08-535-681-25
US-08-535-681-29
US-08-535-681-29
US-08-535-681-32
US-08-535-681-33
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                          GenCore version
Copyright (c) 1993 - 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Sequence

US-08-795-628-1 US-08-519-777-76

arch completed: December 30, 2002, 16:14:04 ob time : 36 secs

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this peptide sequence comprises amino acid residues 9-40 of the human glial cell line-derived neurotrophic factor (GDNF) protein case AMM15705 and represents an N-terminal sequence of a novector case AMM15706 and represents an N-terminal sequence of a novector truncated GDNF. Claimed truncated GDNF proteins have the formula: X-(Cys41-Cys133) - X, where (Cys41-Cys133) - Cys41 through Cys133 of Inclaid through Cys133 of methionylated or nonmethionylated amine group of Cys41 or an N-terminus selected from G, RG, NRG or the N-terminal peptides given in AAW15707-42, and additions, substitutions and internal call of these. Also claimed are: a polynucleotide a transformed or transfected prokaryotic or eukaryotic host cell; and a GDNF composition comprising mature GDNF (see AAW1573); a vector; and a GDNF composition comprising mature GDNF protein (44 kDs) and come or more truncated GDNFs (29-40 kDs). The truncated GDNF is used in the treatment of nervous system damage caused by disease or injury, especially in the treatment of Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Truncated glial cell line-derived neurotrophic factor protein - used in the treatment and gene therapy of Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This peptide sequence comprises amino acid residues 8-40 of the human glial cell line-derived neurotrophic factor (GDNF) protein (see AAMIS706) and represents an N-terminal sequence of a novel truncated GDNF. Claimed truncated GDNF proteins have the formula: X-(Cy441-Cy5133)-Y, where (Cy441-Cy5133) = Cy441 through Cy3133 or mature human GDNF; Y = a C-terminal Cy3133 or Ile134; and X = a methionylated or nonmethionylated amine group of Cy341 or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glial cell line-derived neurotrophic factor; GDNF; human; dopaminergic; nerve cell; Parkinson's disease; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
  in the treatment and gene therapy of Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 104; DB 18;
100.0%; Pred. No. 9.2e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW15736 standard; Peptide; 33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Truncated GDNF N-terminal peptide,
                                                   Claim 1; Page 84; 105pp; English.
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                                                                                                                                                                                                                                                                                                                                               This peptide sequence comprises amino acid residues 10-40 of the human glial cell line-derived neurotrophic factor (GDNF) protein (see AMMISTOR) and represents an N-terminal sequence of a novel truncated GDNF. Claimed truncated GDNF proteins have the formula: X-(Cys41-Cys133)-Y, where (Cys41-Cys133) - Cys41 through Cys133 of mature human GDNF: X = a C-terminal Cys133 or Ilel34; and X = a mature human GDNF: X = a C-terminal Cys133 or Ilel34; and X = a mature human GDNF: X = a C-terminal Gys133 or Ilel34; and X = a mathionylated amine group of Cys41 or an N-terminus selected from G, RG, MRG or the N-terminal peptides given in AAW15707-42, and additions, substitutions and internal claim in AAW15707-45, and additions, substitutions and internal claim in AAW15707-45, encoding a truncated GDNF (see AAW1573-45); a vector; a transformed or transfected prokaryotic or eukaryotic host cell; and a GDNF composition comprising mature GDNF protein (44 kDa) and one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used in the treatment of nervous system damage caused by disease or injury, especially in the treatment of Parkinson's disease.
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100.0%; Pred. No. 9e-08;
11ve 0; Mismatches 0;
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                                                                                          (AMGE-) AMGEN INC.
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16-SEP-1996;
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this peptide sequence comprises amino acid residues 11-40 of the human glial cell line-derived neurotrophic factor (GDNF) protein (see AAWIS706) and represents an N-terminal sequence of a novel truncated GDNF. Claimed truncated GDNF proteins have the formula: X-(Cys41-Cys133) - Cys41-through Cys133 of Incl34; and X = a mature human GDNF; Y = a C.terminal Cys133 or Ile134; and X = a mathionylated or nonmethionylated amine group of Cys41 or an N-terminus selected from G, RG, NRG or the N-terminal peptides given in AAWI5707-42, and additions, substitutions and internal deletion variants of these. Also claimed are: a polynoclectide cee AAMI674-46) encoding a truncated GDNF (see AAMI574-45); a vector; a transformed or transfected prokaryotic or eukaryotic host cell; and a GDNF composition comprising mature GDNF protein (44 kDa) and come or more truncated GDNFs (29-40 kDa). The truncated GDNF is used in the treatment of nervous system damage caused by disease or injury, especially in the treatment of Parkinson's disease.
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                                              Glial cell line-derived neurotrophic factor; GDNF; human; dopaminergic; nerve cell; Parkinson's disease; gene therapy.
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100.0%; Pred. No. 8.7e-08;
ive 0; Mismatches 0;
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X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a methionylated or nonmethionylated amine group of Cys41 or an enthionylated or nonmethionylated amine group of Cys41 or an N-terminus selected from G, RG, NRG or the N-terminal peptides given in AMMISTO7-4.5, and additions, substitutions and internal celetion variants of these. Also claimed are: a polynuclectide deletion variants of these. Also claimed are: a polynuclectide of a transformed or transfected prokaryotic or eukaryotic host cell; and a GDNF composition comprising mature GDNF protein (44 kDa) and one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used in the treatment of nervous system damage caused by disease or contraction comprising the presented GDNF is assed that the treatment of nervous system damage caused by disease or contraction comprised to the presented GDNF is assed that the treatment of partyners of partyners of partyners of partyners.
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11arity 100.0%; Pred. No. 8.4e-08;
Conservative 0; Mismatches 0;
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10 NPENSRGKGRRGQRGKNRG 28
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Length 30; Indels in the treatment of nervous system damage caused by disease or injury, especially in the treatment of Parkinson's disease.

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This peptide sequence comprises amino acid residues 14-40 of the human glial cell line-derived neurotrophic factor (GDNF) protein (SDNF) to see AAW15706) and represents an N-terminal sequence of a novel truncated GDNF. Claimed truncated GDNF proteins have the formula:

X-(Cy841-Cy8133) Y. where (Cy841-Cy8133) = Cy841 through Cy8133 of mature human GDNF; Y = a C-terminal Cy8133 - Cy841 through Cy8133 of mature human GDNF; Y = a C-terminal cy8133 of complex hologylated or nonmethionylated amine group of Cy841 or an methionylated or nonmethionylated amine group of Cy841 or an N-terminal selected from G, RG, NRG or the N-terminal peptides in N-terminal sof these. Also claimed are: a polynucleotide deletion variants of these. Also claimed are: a polynucleotide claim and armiformed or transfered prokaryotto or eukaryotto host cell; and a GDNF composition comprising mature GDNF protein (44 kba) and come or more truncated GDNFs (29-40 kba). The truncated GDNF is used
truncated GDNF. Claimed truncated GDNF proteins have the formula: X-(Cys41-Cys133)-Y, where (Cys41-Cys133) - Cys41 through Cys133 of mature human GDNF; Y - a C-terminal Cys133 or Inel134; and X - a methlonylated or nonmethionylated amine group of Cys41 or an N-terminus selected from G, RG, NRG or the N-terminal peptides given in AAM15707-42, and additions, substitutions and internal deletion variants of these. Also claimed are: a polynucleotide (see AAM5504-46) encoding a truncated GDNF (see AAM15743-45); a vector; a transformed or transfected prokaryotic or eukaryotic host cell; and a GDNF composition comprising mature GDNF protein (44 kba) and one or more truncated GDNFs (29-40 kba). The truncated GDNF is used in the treatment of nervous system damage caused by disease or injury, especially in the treatment of Parkinson's disease.
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100.0%; Pred. No. 7.6e-08;
1ve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                      100.0%;
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les 19; Conservative
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                                                                                                                                                                                                                                                                                          26 AA;
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human glial cell line-derived neurotrophic factor (GDNP) protein (see AAW15706) and represents an N-terminal sequence of a novel truncated GDNF. Claimed truncated GDNF proteins have the formula:

X-(Cy441-Cy9133)-Y. where (Cys41-Cy9133) = Cys41 through Cy9133 of mature human GDNF; Y = a C-terminal Cy8133 or Ile134; and X = a meture human GDNF; Y = a C-terminal Cy8133 or Ile134; and X = a meture human GDNF; Y = a C-terminal Cy8133 or Ile134; and X = a meture human GDNF; Y = a C-terminal Cy8133 or Ile134; and X = a meture human GDNF; Y = a C-terminal Cy8133 or Ile134; and X = a meture human GDNF; Y = a C-terminal Cy8133 or Ile134; and X = a meture human GDNF; Y = a C-terminal Cy8133 or Ile134; and X = a meture human GDNF; Y = a C-terminal Cy8133 or Ile134; and X = a meture human GDNF; Y = a C-terminal Cy8133 or Ile134; and AAW15707-42, and additions, substitutions and internal cy814 or and a CDNF composition conditions, and a GDNF protein (44 kDa) and a GDNF composition comprising mature GDNF protein (44 kDa) and come or more truncated GDNFs (29-40 kDa). The truncated GDNF is used in the treatment of mervous system damage caused by disease or injury, especially in the treatment of Parkinson's disease.
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100.0%; Pred. No. 8.1e-08;
tive 0; Mismatches 0;
                                                                                       Score 104; DB 18;
Pred. No. 7.9e-08;
Mismatches 0;
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This peptide sequence comprises amino acid residues 16-40 of the human glial cell line-derived neurotrophic factor (GDNF) protein (see AAW15706) and represents an N-terminal sequence of a novel truncated GDNF. Claimed truncated GDNF proteins have the formula: X-(Cys41-Cys133) - Cys41-through Cys133 of Incl34; and X = a mature human GDNF; Y = a C-terminal Cys133 or Incl34; and X = a mathionylated or nonmethionylated amine group of Cys41 or an N-terminus selected from G, RG, NRG or the N-terminal peptides given in AAW15707-42, and additions, substitutions and internal celection variants of these. Also claimed are: a polynocleotide (see AAT60542-46) encoding a truncated GDNF (see AAW1573-45); a vector; a transformed or transfected prokaryotic or eukaryotic host cell; and a GDNF composition comprising mature GDNF protein (44 kDa) and one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used in the treatment of nervous system damage caused by disease or injury, especially in the treatment of Parkinson's disease.
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                                                                        Truncated glial cell line-derived neurotrophic factor protein - used in the treatment and gene therapy of Parkinson's disease
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X-(Cys41-Cys133)-Y, where (Cys41-Cys133) - Cys41 through Cys133 of mature human GDNF; Y - a C-terminal Cys133 - Cys41 through Cys133 of mature human GDNF; Y - a C-terminal peptides or nonmethionylated amine group of Cys41 or an ethionylated or nonmethionylated amine group of Cys41 or an ethionylated from G, RG, NRG or the N-terminal peptides of leation variants of these. Also claimed are: a polynucleotide deletion variants of these. Also claimed are: a polynucleotide cleation variants of these. Also claimed are: a polynucleotide at a transformed or transfered prokaryotic or eukaryotic host cell; and a GDNF composition comprising mature GDNF protein (44 kba) and one or more truncated GDNFs (29-d) kba). The truncated GDNF is used that treatment of mervous system damage caused by disease or contraction comparisons of the presented CDNF is the foreign of the treatment of mervous system damage caused by disease or contractions.
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100.0%; Pred. No. 7.1e-08;
ive 0; Mismatches 0;
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human glial cell line-derived neurotrophic factor (GDNF) protein case AMM15705 and represents an N-terminal sequence of a novel truncated GDNF. Claimed truncated GDNF proteins have the formula: truncated GDNF. Claimed truncated GDNF proteins have the formula: X-(Cys41-Cys133) - Cys41 through Cys413 of Lose.

X-(Cys41-Cys133)-Y, where (Cys41-Cys133) - Cys41 through Cys413 of mature human GDNF; Y - a C-terminal Cys133 or Ile134; and X - a methionylated or nonmethionylated amine group of Cys41 or an enthionylated or nonmethionylated amine group of Cys41 or an ethionylated from G, RG, NRG or the N-terminal peptides given in AAM15707-42, and additions, substitutions and internal election variants of these. Also claimed are: a polynucleofilde (see AAT60542-46) encoding a truncated GDNF (see AAM15743-45); a vector; a transformed or transfected prokaryotic or eukaryotic host cell; and GDNF composition comprising mature GDNF protein (44 kDa) and one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used in the treatment of nervous system damage caused by disease or
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100.0%; Pred. No. 6.8e-08;
tive 0; Mismatches 0;
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AAW15727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This peptide sequence comprises amino acid residues 19-40 of the human glial cell line-derived neurotrophic factor (GDNF) protein (see AAMIS706) and represents an N-terminal sequence of a novel truncated GDNF. Claimed truncated GDNF proteins have the formula: X-(Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of mature human GDNF; Y = a C-terminal Cys133 or Ilel34; and X = a methonylated or nonmethionylated amine group of Cys41 or an N-terminal selected from G, RG, NRG or the N-terminal peptides given in AAMIS707-42, and additions, substitutions and internal deletion variants of these. Also claimed are: a polynucleotide (see AAM50542-46) encoding a truncated GDNF (see AAM5743-45); a vector; a transformed or transfected prokaryotic or eukaryotic host cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Truncated glial cell line-derived neurotrophic factor protein - used in the treatment and gene therapy of Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and a GDNF composition comprising mature GDNF protein (44 kDa) and one or more truncated GDNFs (29-40 kDa). The truncated GDNF is used in the treatment of nervous system damage caused by disease or
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                                                                                                                                                                                                                                                                                                                                                           Glial cell line-derived neurotrophic factor; GDNF; human; dopaminergic; nerve cell; Parkinson's disease; gene therapy.
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    Indels
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100.0%; Pred. No. 6.5e-08;
.ive 0; Mismatches 0;
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  Mismatches
                                                                                                                                                                                                                                                                                                                    Truncated GDNF N-terminal peptide.
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                                                                                                                                                                                        AAW15725 standard; Peptide; 22 AA.
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Best Local Similarity 100.
Matches 19; Conservative
Conservative
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19;
                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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RESULT 5 AAW15726

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Length 23; Indels (see AAT60542-46) encoding a truncated GDNF (see AAW15743-45); a vector; a transformed or transfected prokaryotic or eukaryotic host cell; and a GDNF composition comprising mature GDNF protein (44 kba) and one or more truncated GDNFs (29-40 kba). The truncated GDNF is used in the treatment of nervous system damage caused by disease or injury, especially in the treatment of Parkinson's disease.

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Gaps

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Length 20; Indels

100.0%; Score 104; DB 18; 100.0%; Pred. No. 6e-08; ive 0; Mismatches 0;

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case AAM15706) and represents an V-terminal sequence of a novel truncated GDNF. Claimed truncated GDNF proteins have the formula:

X (Cys41-Cys133)-Y, where (Cys41-Cys133) = Cys41 through Cys133 of mature human GDNF; Y = a C-terminal Cys133 or Ile134; and X = a methionylated or nonmethionylated amine group of Cys41 or an methionylated or nonmethionylated amine group of Cys41 or an N-terminus selected from G, RG, NRG or the N-terminal peptides given in AAM15707-42, and additions, substitutions and internal deletion variants of these. Also claimed are: a polynucleotide care AAT60542-46) encoding a truncated GDNF (see AAM16542-45); a vector; a transformed or transfected prokaryotic or eukaryotic host cell; and a GDNF composition comprising mature GDNF protein (44 kba) and con more truncated GDNF (29 40 kba) and the treatment of nervous system damage caused by disease or injury, especially in the treatment of Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Truncated glial cell line-derived neurotrophic factor protein - used in the treatment and gene therapy of Parkinson's disease
               peptide sequence comprises amino acid residues 22-40 of the
                              human gilal celi line-derived neurotrophic factor (GDNF) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glial cell line-derived neurotrophic factor; GDNF; human; dopaminergic; nerve cell; Parkinson's disease; gene therapy.
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                                                                                                                                                                                                                                                                                                                        100.0%; Score 104; DB 18;
100.0%; Pred. No. 5.7e-08;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Truncated GDNF N-terminal peptide.
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                           19 AA;
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Glial cell line-derived neurotrophic factor; GDNF; human; dopaminergic; nerve cell; Parkinson's disease; gene therapy.

96WO-US14915.

16-SEP-1996; 28-SEP-1995;

03-APR-1997.

W09711964-A1

Synthetic.

95US-0535681

(AMGE-) AMGEN INC.

Truncated GDNF N-terminal peptide.

(first entry)

28-NOV-1997

AAW15724;

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Gaps

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AAW15724 standard; Peptide; 21 AA.

RESULT 3

2 NPENSRGKGRRGQRGKNRG 20

1 NPENSRGKGRRGQRGKNRG 19

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Local Similarity 100. nes 19; Conservative

Best

20 AA;

Sequence Query Match Matches

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This peptide sequence comprises amino acid residues 20-40 of the human gilal cell line-derived neurotrophic factor (GDNF) protein case AAM15706) and represents an N-terminal sequence of a novel truncated GDNF. Claimed truncated GDNF proteins have the formula:

X-(Cy41-Cy313)-Y, where (Cy541-Cy5133) = Cy41 through Cy5133 of mature human GDNF; Y = a C-terminal Cy5133 or Ile134; and X = a methionylated or nonmethionylated amine group of Cy541 or an entionylated connomethionylated amine group of Cy541 or an entionylated from G, RG, NRG or the N-terminal peptides of year in AAW15707-42, and additions, substitutions and internal deletion variants of these. Also claimed are: a polynucleotide (see AAT60542-46) encoding a truncated GDNF (see AW15743-45); a vector; a transformed or transfected prokaryotic or eukaryotic host cell; and a GDNF composition comprising mature GDNF protein (44 kba) and contracted GDNFs (29-40 kba). The truncated GDNF is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Truncated glial cell line-derived neurotrophic factor protein - used in the treatment and gene therapy of Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 one or more truncated GDNFs (29-40 kDa). The truncated GDNF is in the treatment of nervous system damage caused by disease or injury, especially in the treatment of Parkinson's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 83; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-212849/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AA;
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This peptide sequence comprises amino acid residues 21-40 of the human glial cell line-derived neurotrophic factor (GDNF) protein (see AAM15706) and represents an N-terminal sequence of a novel truncated GDNF. Claimed truncated GDNF proteins have the formula: X-(Cy841-Cy8133)-Y, where (Cy841-Cy8133)-Cy841 through Cy8133 of mature human GDNF; Y = a C-terminal Cy813 or Ile134; and X = a methonylated or nonmethionylated amine group of Cy841 or an methonylated from G, RG, NRG or the N-terminal peptides given in AAW15707-42, and addittions, substitutions and internal deletion variants of these. Also claimed are: a polynucleotide

Claim 1; Page 83; 105pp; English.

Score 104; DB 18; Pred. No. 6.2e-08; 100.0%; Query Match Best Local Similarity

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Tue Dec 31 09:05:13 2002
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December 30, 2002, 15:36:42; Search time 35 Seconds (without alignments) 72.336 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                            OM protein - protein search, using sw model
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US-09-687-993-18 104 1 NPENSRGKGRRGQRGKNRG 19 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Title: Perfect score:

Sequence:

otal number of hits satisfying chosen parameters: 908470 segs, 133250620 residues earched:

908470

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

// SIDSZ/gcddata/geneseq/geneseqp-embl/Aa1980.DAT:*
// SIDSZ/gcddata/geneseqy/geneseqp-embl/Aa1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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e	104	100.0	21	18	AAW15724		
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ß	104	100.0	23	18	AAW15726	GDNF	
9	104	100.0	24	18	AAW15727		
7	104	100.0	25	18	AAW15728	GDNF	
80	104	100.0	56	18	AAW15729	GDNF	
σ	104	100.0	27	18	AAW15730	GDNF	
. 10	104	100.0	28	18	AAW15731	Truncated GDNF N-t	

Claim 1; Page 83; 105pp; English.

Truncated GDNF N-t	z	GDNF	Truncated GDNF N-t	Truncated GDNF N-t	Truncated GDNF N-t	Truncated CDNF N-t	Truncated GDNF N-t			Human ATF-2, Homo	Human glial-derive	=	O,	e human	Glial cell derived	Human mature glial	Glial cell line-de	ശ	GDNF amino acid se	Human TGFbeta prot	Human glial cell l	Human glial cell 1	Human GDNF protein	_	Human ATF-1. Homo	14	Human glial cell l		Ē.	S	WO9914235 Sed ID N	Rat GDNF polypept1	mutan
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50	3 1	32	33	34	35	36	37	38	39	133	133	134	134	134	134	134	134	134	134	134	135	135	159	160	185	185	211	211	211	134	134	134	147
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ALIGNMENTS

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Truncated glial cell line-derived neurotrophic factor protein - used in the treatment and gene therapy of Parkinson's disease
                                                                             Glial cell line-derived neurotrophic factor; GDNF; human; dopaminergic; nerve cell; Parkinson's disease; gene therapy.
AAW15722 standard; Peptide; 19 AA.
                                                          Truncated GDNF N-terminal peptide.
                                                                                                                                                                    96WO-US14915.
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                                       28-NOV-1997 (first entry)
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                                                                                                                                                                                                         (AMGE-) AMGEN INC.
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                                                                                                                                                                                       28-SEP-1995;
                                                                                                                                                 03-APR-1997.
                                                                                                           Synthetic.
                   AAW15722;
                                                                                                                                                                                                                             Hu SS;
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